REMARKS

Upon entry of the Amendment, claims 14 to 27, 29 to 30, and 43 to 66 are pending in the application. The specification is amended. Claims 1 to 13, 28, and 31 to 42 are canceled. Claims 14 to 27 are withdrawn from consideration. Claims 14 to 17, 21 to 27, and 29 to 30 are amended. Claims 43 to 66 are new.

No new matter is added. Withdrawn claim 14 is amended for the purpose of a possible rejoinder thereof. Withdrawn claims 15 and 16 are amended, in view of the amendment to withdrawn claim 14. Withdrawn claims 21 to 27 are amended in view of the cancellation of claims 1 to 13. The specification supports the amendments to claims 29 and 30, such as on pages 7 to 9. The specification supports new claims 43 to 66, such as on pages 7 to 9. Entry of the amendment is respectfully requested.

I. Election/Restriction

Referring to pages 2 to 3 of the Office Action, the Examiner asserts that Groups XXXI, X, XI, and XII do not share the same technical feature.

Applicants respectfully submit that the examination of Groups XXXI, X, XI, and XII would not result in an unduly burdensome search. Example 4 of the present specification discloses that each of SEQ ID NO: 4, SEQ ID NO: 7, and SEQ ID NO: 10 differ from the amino acid sequence of SEQ ID NO: 1 by one amino acid.

II. Specification

The specification is objected to allegedly because of the use of improperly demarcated trademarks.

The specification is amended in an effort to refer to trademarks.

III. Claim Rejections - 35 U.S.C. § 112

(A) Claims 29 and 30 are rejected under 35 U.S.C. § 112, second paragraph, as allegedly being indefinite.

The Examiner asserts that the phrase "the same or substantially is indefinite the same amino acid sequence as the amino acid sequence represented by SEQ ID NO: 1."

Claims 29 and 30 are amended. Applicants respectfully submit that a person skilled in the art can understand the metes and bounds of claims 29 and 30, as presently recited.

(B) Claims 29 to 30 are rejected under 35 U.S.C. § 112, first paragraph, as allegedly failing to comply with the written description requirement.

The Examiner asserts that the specification fails to provide written description support for a protein having "substantially the same" amino acid sequence as the amino acid sequence of SEQ ID NO: 1 or the claimed partial peptide. The Examiner asserts that a person skilled in the art could not immediately envision, recognize or distinguish most of the members of the genus.

Applicants respectfully submit that the specification provides written description support to amended claims 29 and 30. Page 9 of the specification describes that the protein may have 1 to 10 substitutions, deletions, or insertions. Example 8 of the specification also describes producing antibodies with peptides having the amino acid sequence present at position 402 to 412 of SEQ ID NO: 1, 582 to 596 of SEQ ID NO: 1, 781 to 794 of SEQ ID NO: 1, and 797 to 809 of SEQ ID NO: 1. *See* Example 8 of the Specification. Further, the specification provides the amino acid sequences of SEQ ID NOs: 4, 7, and 10. SEQ ID NO: 4 differs from SEQ ID NO: 1 at position 208. SEQ ID NO: 7 differs from SEQ ID NO: 1 at position 163. SEQ ID NO: 10 differs from SEQ ID NO: 1 at position 364.

In view of the above descriptions, a person skilled in the art can predict the amino acid sequence of an amino acid sequence in which 1 to 10 amino acid sequences have been substituted, deleted or inserted into SEQ ID NO: 1, wherein said substitution, deletion, or insertion is with an amino acid position outside of position 402 to 412 of SEQ ID NO: 1, 582 to 596 of SEQ ID NO: 1, 781 to 794 of SEQ ID NO: 1, and 797 to 809 of SEQ ID NO: 1. The amino acid sequence indicates which positions may include the substitution, deletion, or insertions of 1 to 10 amino acids. Example 8 describes using peptides having the amino acids at positions 402 to 412, 582 to 596, 781 to 794, and 797 to 809 of SEQ ID NO: 1 to produce the antibodies thereof. The specification provides examples of such an amino acid sequence in SEQ ID NOs: 4, 7, and 10. In this regard, the specification provides written description support to amended claims 29 and 30.

IV. Claim Rejections - 35 U.S.C. § 102

The Office Action contains two rejections under 35 U.S.C. § 102, as follows:

> claims 29 to 30 are rejected under 35 U.S.C. § 102(b) as allegedly being anticipate by Osada et al.; and
>
> claims 29 and 30 are rejected under 35 U.S.C. § 102(b) as allegedly being anticipated by Cuello et al.

With respect to Osada, the Examiner asserts that Osada discloses an antiphosphotyrosine monoclonal antibody that specifically binds to phosphotyrosine amino acids. The Examiner asserts that SEQ ID NO: 1 includes multiple tyrosine residues.

Applicants respectfully submit that Osada fails to describe or suggest an antibody that specifically binds to the claimed proteins. Figure 2 of Osada indicates that the antiphosphotryrosine antibody thereof unspecifically binds to proteins including phosphotyrosine amino acids. In this regard, Figure 2 of Osada indicates that the antiphosphotyrosine antibody

thereof may bind to proteins that do not comprise the amino acid sequence of SEQ ID NO: 1 or to proteins in which one to ten amino acids have deleted from, inserted into, or substituted inot the amino acid sequence of SEQ ID NO: 1, wherein said deletion, insertion, or substitution occurs at an amino acid position outside of positions 402 to 412 of SEQ ID NO: 1, 582 to 596 of SEQ ID NO: 1, 781 to 794 of SEQ ID NO: 1, and 797 to 809 of SEQ ID NO: 1. More than a phospotyrosine amino acid, if any, is present at positions 402 to 412, 582 to 596, 781 to 794, and 797 to 809 of SEQ ID NO: 1. In this regard, the antiphospotyrosine antibody is not specific to the proteins recited in claims 29 and 30.

With respect to Cuello, the Examiner asserts that Cuello describes an antibody that binds to an erbB-2 polypeptide (i.e., trastuzumab). The Examiner asserts that the protein recited in claims 29 and 30 would encompass erbB-2 as disclosed in Cuello.

Applicants Cuello fails to expressly describe the amino acid sequence of the erbB-2 polypeptide thereof. Cuello discloses using erbB-2 from several cell lines (SKBr-3, MDA-MB-453, SKOv-3, MDA-MB-468, SW-626, MDA-MB-231, and MCF-7). *See* Cuello, p. 4892-4893. GENBANK™ provides the amino acid sequence of Receptor tyrosine-protein kinase erbB-2 precursor (p185erbB2). A copy of the amino acid sequence is provided herewith. Based on a comparison with the Receptor tyrosine-protein kinase erbB-2, it appears that amino acid sequences of the claimed proteins are significantly different. In this regard, the antibody disclosed in Cuello is different from the antibody recited in claims 29 and 30.

V. Double Patenting

Claims 29-30 are provisionally rejected on the ground of nonstatutory obviousness-type double patenting, as allegedly being unpatentable over claims 1-14 of copending Application no. 10/584,183.

Applicants defer responding at this time to this provisional obviousness-type double patenting rejection, pursuant to MPEP § 804(I)(B).

In view of the above, reconsideration and allowance of this application are now believed to be in order, and such actions are hereby solicited. If any points remain in issue which the Examiner feels may be best resolved through a personal or telephone interview, the Examiner is kindly requested to contact the undersigned at the telephone number listed below.

The USPTO is directed and authorized to charge all required fees, except for the Issue Fee and the Publication Fee, to Deposit Account No. 19-4880. Please also credit any overpayments to said Deposit Account.

Respectfully submitted,

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WASHINGTON OFFICE
23373
CUSTOMER NUMBER

Date: October 18, 2007

1: P04626. Reports Receptor tyrosine...[gi:119533]

BLink, Conserved Domains, Links

Comment Features Sequence

```
LOCUS       P04626                  1255 aa            linear   PRI 10-JUL-2007
DEFINITION  Receptor tyrosine-protein kinase erbB-2 precursor (p185erbB2)
            (C-erbB-2) (NEU proto-oncogene) (Tyrosine kinase-type cell surface
            receptor HER2) (MLN 19) (CD340 antigen).
ACCESSION   P04626
VERSION     P04626  GI:119533
DBSOURCE    swissprot: locus ERBB2_HUMAN, accession P04626;
            class: standard.
            extra accessions:Q14256,Q6LDV1,Q9UMK4
            created: Aug 13, 1987.
            sequence updated: Aug 13, 1987.
            annotation updated: Jul 10, 2007.
            xrefs: M11767.1, AAA35808.1, M11761.1, M11762.1, M11763.1,
            M11764.1, M11765.1, M11766.1, M11730.1, AAA75493.1, M12036.1,
            AAA35978.1, AY208911.1, AAO18082.1, X03363.1, CAA27060.1, M16792.1,
            AAA58637.1, M16789.1, M16790.1, M16791.1, L29395.1, AAA35809.1,
            M95667.1, AAC37531.1, A24571, 1N8ZC, 1OVC_A, 1QR1F, 1S78A, 1S78B,
            2A91A
            xrefs (non-sequence databases): UniGene:Hs.446352, DIP:DIP:8N,
            IntAct:P04626, Ensembl:ENSG00000141736, KEGG:hsa:2064, HGNC:3430,
            HPA:CAB000043, HPA:HPA001383, MIM: 164870, PharmGKB:PA27844,
            DrugBank:BTD00098, LinkHub:P04626, ArrayExpress:P04626,
            GermOnline:ENSG00000141736, RZPD-ProtExp:B0017, GO:0016021,
            GO:0005886, GO:0005006, GO:0043125, GO:0042802, GO:0046982,
            GO:0004716, GO:0007507, GO:0030879, GO:0007399, GO:0048015,
            GO:0050679, GO:0043406, GO:0006468, GO:0045765, GO:0007169,
            InterPro:IPR000494, InterPro:IPR006211, InterPro:IPR006212,
            InterPro:IPR000719, InterPro:IPR001245, InterPro:IPR008266,
            InterPro:IPR004019, Pfam:PF00757, Pfam:PF07714, Pfam:PF01030,
            Pfam:PF02757, PRINTS:PR00109, ProDom:PD000001, SMART:SM00261,
            SMART:SM00219, PROSITE:PS00107, PROSITE:PS50011, PROSITE:PS00109
KEYWORDS    3D-structure; ATP-binding; Glycoprotein; Kinase; Membrane;
            Nucleotide-binding; Phosphorylation; Polymorphism; Receptor;
            Signal; Transferase; Transmembrane; Tyrosine-protein kinase.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
REFERENCE   1  (residues 1 to 1255)
  AUTHORS   Yamamoto,T., Ikawa,S., Akiyama,T., Semba,K., Nomura,N.,
            Miyajima,N., Saito,T. and Toyoshima,K.
  TITLE     Similarity of protein encoded by the human c-erb-B-2 gene to
            epidermal growth factor receptor
  JOURNAL   Nature 319 (6050), 230-234 (1986)
   PUBMED   3003577
```

REMARK NUCLEOTIDE SEQUENCE [MRNA].
REFERENCE 2 (residues 1 to 1255)
AUTHORS Coussens,L., Yang-Feng,T.L., Liao,Y.C., Chen,E., Gray,A., McGrath,J., Seeburg,P.H., Libermann,T.A., Schlessinger,J., Francke,U., Levinson,A. and Ullrich,A.
TITLE Tyrosine kinase receptor with extensive homology to EGF receptor shares chromosomal location with neu oncogene
JOURNAL Science 230 (4730), 1132-1139 (1985)
PUBMED 2999974
REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA], AND VARIANT ALA-1170.
REFERENCE 3 (residues 1 to 1255)
AUTHORS Rieder,M.J., Livingston,R.J., Daniels,M.R., Montoya,M.A., Chung,M.-W., Miyamoto,K.E., Nguyen,C.P., Nguyen,D.A., Poel,C.L., Robertson,P.D., Schackwitz,W.S., Sherwood,J.K., Witrak,L.A. and Nickerson,D.A.
TITLE Direct Submission
JOURNAL Submitted (??-DEC-2002)
REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS CYS-452; VAL-655 AND ALA-1170.
REFERENCE 4 (residues 1 to 1255)
AUTHORS Tal,M., King,C.R., Kraus,M.H., Ullrich,A., Schlessinger,J. and Givol,D.
TITLE Human HER2 (neu) promoter: evidence for multiple mechanisms for transcriptional initiation
JOURNAL Mol. Cell. Biol. 7 (7), 2597-2601 (1987)
PUBMED 3039351
REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-191.
REFERENCE 5 (residues 1 to 1255)
AUTHORS Semba,K., Kamata,N., Toyoshima,K. and Yamamoto,T.
TITLE A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epidermal growth factor-receptor gene and is amplified in a human salivary gland adenocarcinoma
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 82 (19), 6497-6501 (1985)
PUBMED 2995967
REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 737-1031.
REFERENCE 6 (residues 1 to 1255)
AUTHORS King,C.R., Kraus,M.H. and Aaronson,S.A.
TITLE Amplification of a novel v-erbB-related gene in a human mammary carcinoma
JOURNAL Science 229 (4717), 974-976 (1985)
PUBMED 2992089
REMARK NUCLEOTIDE SEQUENCE OF 832-909.
TISSUE=Mammary carcinoma
REFERENCE 7 (residues 1 to 1255)
AUTHORS Sarkar,F.H., Ball,D.E., Li,Y.W. and Crissman,J.D.
TITLE Molecular cloning and sequencing of an intron of Her-2/neu (ERBB2) gene
JOURNAL DNA Cell Biol. 12 (7), 611-615 (1993)
PUBMED 8104414
REMARK NUCLEOTIDE SEQUENCE OF 1081-1245, AND VARIANT ALA-1170.
REFERENCE 8 (residues 1 to 1255)
AUTHORS Arcaro,A., Zvelebil,M.J., Wallasch,C., Ullrich,A., Waterfield,M.D. and Domin,J.
TITLE Class II phosphoinositide 3-kinases are downstream targets of activated polypeptide growth factor receptors
JOURNAL Mol. Cell. Biol. 20 (11), 3817-3830 (2000)
PUBMED 10805725
REMARK IDENTIFICATION IN A COMPLEX WITH PIK3C2A AND EGFR, IDENTIFICATION IN A COMPLEX WITH PIK3C2B AND EGFR, AND INTERACTION WITH PIK3C2B.
REFERENCE 9 (residues 1 to 1255)
AUTHORS Swiercz,J.M., Kuner,R. and Offermanns,S.
TITLE Plexin-B1/RhoGEF-mediated RhoA activation involves the receptor tyrosine kinase ErbB-2
JOURNAL J. Cell Biol. 165 (6), 869-880 (2004)

PUBMED 15210733
REMARK INTERACTION WITH PLXNB1.
REFERENCE 10 (residues 1 to 1255)
AUTHORS Marone,R., Hess,D., Dankort,D., Muller,W.J., Hynes,N.E. and Badache,A.
TITLE Memo mediates ErbB2-driven cell motility
JOURNAL Nat. Cell Biol. 6 (6), 515-522 (2004)
PUBMED 15156151
REMARK INTERACTION WITH MEMO.
REFERENCE 11 (residues 1 to 1255)
AUTHORS Olsen,J.V., Blagoev,B., Gnad,F., Macek,B., Kumar,C., Mortensen,P. and Mann,M.
TITLE Global, in vivo, and site-specific phosphorylation dynamics in signaling networks
JOURNAL Cell 127 (3), 635-648 (2006)
PUBMED 17081983
REMARK PHOSPHORYLATION [LARGE SCALE ANALYSIS] AT TYR-1248, AND MASS SPECTROMETRY.
TISSUE=Epithelium
REFERENCE 12 (residues 1 to 1255)
AUTHORS Kuhns,J.J., Batalia,M.A., Yan,S. and Collins,E.J.
TITLE Poor binding of a HER-2/neu epitope (GP2) to HLA-A2.1 is due to a lack of interactions with the center of the peptide
JOURNAL J. Biol. Chem. 274 (51), 36422-36427 (1999)
PUBMED 10593938
REMARK X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 654-662 IN COMPLEX WITH HLA AND BETA-2 MICROGLOBULIN.
REFERENCE 13 (residues 1 to 1255)
AUTHORS Cho,H.S., Mason,K., Ramyar,K.X., Stanley,A.M., Gabelli,S.B., Denney,D.W. Jr. and Leahy,D.J.
TITLE Structure of the extracellular region of HER2 alone and in complex with the Herceptin Fab
JOURNAL Nature 421 (6924), 756-760 (2003)
PUBMED 12610629
REMARK X-RAY CRYSTALLOGRAPHY (2.52 ANGSTROMS) OF 23-629 IN COMPLEX WITH FAB.
REFERENCE 14 (residues 1 to 1255)
AUTHORS Ehsani,A., Low,J., Wallace,R.B. and Wu,A.M.
TITLE Characterization of a new allele of the human ERBB2 gene by allele-specific competition hybridization
JOURNAL Genomics 15 (2), 426-429 (1993)
PUBMED 8095488
REMARK VARIANTS VAL-654 AND VAL-655.
COMMENT On Mar 15, 2005 this sequence version replaced gi:86984.
[FUNCTION] Essential component of a neuregulin-receptor complex, although neuregulins do not interact with it alone. GP30 is a potential ligand for this receptor. Not activated by EGF, TGF-alpha and amphiregulin.
[CATALYTIC ACTIVITY] ATP + a [protein]-L-tyrosine = ADP + a [protein]-L-tyrosine phosphate.
[SUBUNIT] Heterodimer with each of the other ERBB receptors (Potential). Interacts with PRKCABP and PLXNB1. Part of a complex with EGFR and either PIK3C2A or PIK3C2B. May interact with PIK3C2B when phosphorylated on Tyr-1196. Interacts with MEMO when phosphorylated on Tyr-1248.
[INTERACTION] Self; NbExp=1; IntAct=EBI-641062, EBI-641062; P62157:CALM (xeno); NbExp=1; IntAct=EBI-641062, EBI-397403; P62161:Calm1 (xeno); NbExp=1; IntAct=EBI-641062, EBI-397530; P00533:EGFR; NbExp=2; IntAct=EBI-641062, EBI-297353; P21860:ERBB3; NbExp=4; IntAct=EBI-641062, EBI-720706; Q15303:ERBB4; NbExp=2; IntAct=EBI-641062, EBI-80371.
[SUBCELLULAR LOCATION] Membrane; Single-pass type I membrane protein.
[PTM] Ligand-binding increases phosphorylation on tyrosine residues

(By similarity).
[POLYMORPHISM] There are fours alleles due to the variations in positions 654 and 655. Allele B1 (Ile-654/Ile-655) has a frequency of 0.782; allele B2 (Ile-654/Val-655) has a frequency of 0.206; allele B3 (Val-654/Val-655) has a frequency of 0.012.
[SIMILARITY] Belongs to the Tyr protein kinase family. EGF receptor subfamily.
[SIMILARITY] Contains 1 protein kinase domain.
[WEB RESOURCE] NAME=Atlas of Genetics and Cytogenetics in Oncology and Haematology;
URL='http://atlasgeneticsoncology.org/Genes/ERBB2ID162ch17q11.html'
.
[WEB RESOURCE] NAME=Wikipedia ERBB2 entry;
URL='http://en.wikipedia.org/wiki/ERBB2'.

FEATURES	Location/Qualifiers
source	1..1255 /organism="Homo sapiens" /db_xref="taxon:9606"
gene	1..1255 /gene="ERBB2" /note="synonyms: HER2, NEU, NGL"
Protein	1..1255 /gene="ERBB2" /product="Receptor tyrosine-protein kinase erbB-2 precursor" /EC_number="2.7.10.1"
Region	1..22 /gene="ERBB2" /region_name="Signal" /inference="non-experimental evidence, no additional details recorded" /note="Potential."
Region	23..1255 /gene="ERBB2" /region_name="Mature chain" /experiment="experimental evidence, no additional details recorded" /note="Receptor tyrosine-protein kinase erbB-2. /FTId=PRO_0000016669."
Region	23..652 /gene="ERBB2" /region_name="Topological domain" /inference="non-experimental evidence, no additional details recorded" /note="Extracellular (Potential)."
Region	25..27 /gene="ERBB2" /region_name="Beta-strand region" /experiment="experimental evidence, no additional details recorded"
Region	39..50 /gene="ERBB2" /region_name="Helical region" /experiment="experimental evidence, no additional details recorded"
Region	52..173 /gene="ERBB2" /region_name="Recep_L_domain" /note="Receptor L domain. The L domains from these receptors make up the bilobal ligand binding site. Each L domain consists of a single-stranded right hand beta-helix. This Pfam entry is missing the first 50 amino acid residues of the domain; pfam01030" /db_xref="CDD:79745"

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Site            68
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                /inference="non-experimental evidence, no additional
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                /note="N-linked (GlcNAc...) (Potential)."
Region          72..74
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Region          79..82
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                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
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Region          84..88
                /gene="ERBB2"
                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
Region          109..111
                /gene="ERBB2"
                /region_name="Hydrogen bonded turn"
                /experiment="experimental evidence, no additional details
                recorded"
Region          112..117
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                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
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Site            124
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                /inference="non-experimental evidence, no additional
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                /note="N-linked (GlcNAc...) (Potential)."
Region          152..157
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Region          164..166
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                /region_name="Hydrogen bonded turn"
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Region          175..177
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Region          182..184
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     Region     189..343
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                /region_name="Furin-like"
                /note="Furin-like cysteine rich region; pfam00757"
                /db_xref="CDD:64613"
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                /inference="non-experimental evidence, no additional
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     Bond       bond(199,212)
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                /bond_type="disulfide"
                /inference="non-experimental evidence, no additional
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                /note="By similarity."
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     Region     217..219
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                /inference="non-experimental evidence, no additional
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                /note="By similarity."
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                /region_name="Beta-strand region"
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                /note="Furin-like repeats. Cysteine rich region. Exact
                function of the domain is not known. Furin is a
                serine-kinase dependent proprotein processor. Other
                members of this family include endoproteases and cell
                surface receptors; cd00064"
                /db_xref="CDD:28946"
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                /bond_type="disulfide"
                /inference="non-experimental evidence, no additional
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                /note="By similarity."
     Bond       bond(240,252)
                /gene="ERBB2"
                /bond_type="disulfide"
                /inference="non-experimental evidence, no additional
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                /note="By similarity."
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                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
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     Region     244..248
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                /experiment="experimental evidence, no additional details
                recorded"
     Region     251..260
                /gene="ERBB2"
                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Bond       bond(255,264)
                /gene="ERBB2"
                /bond_type="disulfide"
                /inference="non-experimental evidence, no additional
                details recorded"
                /note="By similarity."
     Site       259
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                /inference="non-experimental evidence, no additional
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                /note="N-linked (GlcNAc...) (Potential)."
     Region     263..267
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                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
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     Bond       bond(268,295)
                /gene="ERBB2"
                /bond_type="disulfide"
                /inference="non-experimental evidence, no additional
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                /note="By similarity."
     Region     271..274
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     Region     276..278
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                /experiment="experimental evidence, no additional details
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                /gene="ERBB2"
                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     289..291
                /gene="ERBB2"
                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     294..298
                /gene="ERBB2"
                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Bond       bond(299,311)
                /gene="ERBB2"
                /bond_type="disulfide"
                /inference="non-experimental evidence, no additional
                details recorded"
                /note="By similarity."
     Region     303..305
                /gene="ERBB2"
                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     309..314
                /gene="ERBB2"
                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Bond       bond(315,331)
                /gene="ERBB2"
                /bond_type="disulfide"
                /inference="non-experimental evidence, no additional
                details recorded"
                /note="By similarity."
     Region     319..323
                /gene="ERBB2"
                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     329..333
                /gene="ERBB2"
                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Bond       bond(334,338)
                /gene="ERBB2"
                /bond_type="disulfide"
                /inference="non-experimental evidence, no additional
                details recorded"
                /note="By similarity."
     Region     335..337
                /gene="ERBB2"
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                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     348..350
                /gene="ERBB2"
                /region_name="Helical region"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     358..360
                /gene="ERBB2"
                /region_name="Hydrogen bonded turn"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     361..364
                /gene="ERBB2"
                /region_name="Helical region"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     366..486
                /gene="ERBB2"
                /region_name="Recep_L_domain"
                /note="Receptor L domain. The L domains from these
                receptors make up the bilobal ligand binding site. Each L
                domain consists of a single-stranded right hand
                beta-helix. This Pfam entry is missing the first 50 amino
                acid residues of the domain; pfam01030"
                /db_xref="CDD:79745"
     Region     368..376
                /gene="ERBB2"
                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     378..380
                /gene="ERBB2"
                /region_name="Helical region"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     396..402
                /gene="ERBB2"
                /region_name="Helical region"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     405..408
                /gene="ERBB2"
                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     410..413
                /gene="ERBB2"
                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     423..425
                /gene="ERBB2"
                /region_name="Helical region"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     438..440
                /gene="ERBB2"
                /region_name="Hydrogen bonded turn"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     441..447
                /gene="ERBB2"
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                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     452
                /gene="ERBB2"
                /region_name="Variant"
                /experiment="experimental evidence, no additional details
                recorded"
                /note="W -> C. /FTId=VAR_016317."
     Region     463..469
                /gene="ERBB2"
                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     482..485
                /gene="ERBB2"
                /region_name="Helical region"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     493..498
                /gene="ERBB2"
                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     501..506
                /gene="ERBB2"
                /region_name="Helical region"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     509..544
                /gene="ERBB2"
                /region_name="FU"
                /note="Furin-like repeats; smart00261"
                /db_xref="CDD:47590"
     Bond       bond(511,520)
                /gene="ERBB2"
                /bond_type="disulfide"
                /inference="non-experimental evidence, no additional
                details recorded"
                /note="By similarity."
     Bond       bond(515,528)
                /gene="ERBB2"
                /bond_type="disulfide"
                /inference="non-experimental evidence, no additional
                details recorded"
                /note="By similarity."
     Region     516..518
                /gene="ERBB2"
                /region_name="Helical region"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     520..524
                /gene="ERBB2"
                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     528..536
                /gene="ERBB2"
                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Site       530
                /gene="ERBB2"
                /site_type="glycosylation"
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                /inference="non-experimental evidence, no additional
                details recorded"
                /note="N-linked (GlcNAc...) (Potential)."
     Bond       bond(531,540)
                /gene="ERBB2"
                /bond_type="disulfide"
                /inference="non-experimental evidence, no additional
                details recorded"
                /note="By similarity."
     Region     539..542
                /gene="ERBB2"
                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Bond       bond(544,560)
                /gene="ERBB2"
                /bond_type="disulfide"
                /inference="non-experimental evidence, no additional
                details recorded"
                /note="By similarity."
     Region     545..551
                /gene="ERBB2"
                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     553..556
                /gene="ERBB2"
                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     557..603
                /gene="ERBB2"
                /region_name="FU"
                /note="Furin-like repeats; smart00261"
                /db_xref="CDD:47590"
     Region     559..562
                /gene="ERBB2"
                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Bond       bond(563,576)
                /gene="ERBB2"
                /bond_type="disulfide"
                /inference="non-experimental evidence, no additional
                details recorded"
                /note="By similarity."
     Bond       bond(567,584)
                /gene="ERBB2"
                /bond_type="disulfide"
                /inference="non-experimental evidence, no additional
                details recorded"
                /note="By similarity."
     Region     571..573
                /gene="ERBB2"
                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Site       571
                /gene="ERBB2"
                /site_type="glycosylation"
                /inference="non-experimental evidence, no additional
                details recorded"
                /note="N-linked (GlcNAc...) (Potential)."
     Region     575..580
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                /gene="ERBB2"
                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     583..592
                /gene="ERBB2"
                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Bond       bond(587,596)
                /gene="ERBB2"
                /bond_type="disulfide"
                /inference="non-experimental evidence, no additional
                details recorded"
                /note="By similarity."
     Region     595..599
                /gene="ERBB2"
                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Bond       bond(600,623)
                /gene="ERBB2"
                /bond_type="disulfide"
                /inference="non-experimental evidence, no additional
                details recorded"
                /note="By similarity."
     Region     615..617
                /gene="ERBB2"
                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     621..625
                /gene="ERBB2"
                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Bond       bond(626,634)
                /gene="ERBB2"
                /bond_type="disulfide"
                /inference="non-experimental evidence, no additional
                details recorded"
                /note="By similarity."
     Site       629
                /gene="ERBB2"
                /site_type="glycosylation"
                /inference="non-experimental evidence, no additional
                details recorded"
                /note="N-linked (GlcNAc...) (Potential)."
     Bond       bond(630,642)
                /gene="ERBB2"
                /bond_type="disulfide"
                /inference="non-experimental evidence, no additional
                details recorded"
                /note="By similarity."
     Region     653..675
                /gene="ERBB2"
                /region_name="Transmembrane region"
                /inference="non-experimental evidence, no additional
                details recorded"
                /note="Potential."
     Region     654
                /gene="ERBB2"
                /region_name="Variant"
                /experiment="experimental evidence, no additional details
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recorded"
/note="I -> V (in allele B3; dbSNP:rs1801201).
/FTId=VAR_004077."

Region 655
/gene="ERBB2"
/region_name="Variant"
/experiment="experimental evidence, no additional details recorded"
/note="I -> V (in allele B2 and allele B3; dbSNP:rs1801200). /FTId=VAR_004078."

Region 676..1255
/gene="ERBB2"
/region_name="Topological domain"
/inference="non-experimental evidence, no additional details recorded"
/note="Cytoplasmic (Potential)."

Region 715..979
/gene="ERBB2"
/region_name="TyrKc"
/note="Tyrosine kinase, catalytic domain. Phosphotransferases; tyrosine-specific kinase subfamily; cd00192"
/db_xref="CDD:29154"

Region 720..987
/gene="ERBB2"
/region_name="Domain"
/experiment="experimental evidence, no additional details recorded"
/note="Protein kinase."

Region 720..972
/gene="ERBB2"
/region_name="S_TKc"
/note="Serine/Threonine protein kinases, catalytic domain; Phosphotransferases. Serine or threonine-specific kinase subfamily; smart00220"
/db_xref="CDD:47550"

Site 726..734
/gene="ERBB2"
/site_type="np-binding"
/inference="non-experimental evidence, no additional details recorded"
/note="ATP (By similarity)."

Region 742..745
/gene="ERBB2"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Region 748..753
/gene="ERBB2"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Site 753
/gene="ERBB2"
/site_type="binding"
/inference="non-experimental evidence, no additional details recorded"
/note="ATP (By similarity)."

Region 761..776
/gene="ERBB2"
/region_name="Helical region"
/experiment="experimental evidence, no additional details recorded"

Site order(783,798..805,849..850,862..864)

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                /gene="ERBB2"
                /site_type="other"
                /note="ATP binding pocket"
                /db_xref="CDD:29154"
     Region     785..799
                /gene="ERBB2"
                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     806..812
                /gene="ERBB2"
                /region_name="Helical region"
                /experiment="experimental evidence, no additional details
                recorded"
     Site       order(807,845,849,882..886)
                /gene="ERBB2"
                /site_type="other"
                /note="peptide substrate binding pocket"
                /db_xref="CDD:29154"
     Region     814..816
                /gene="ERBB2"
                /region_name="Helical region"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     819..838
                /gene="ERBB2"
                /region_name="Helical region"
                /experiment="experimental evidence, no additional details
                recorded"
     Site       843..852
                /gene="ERBB2"
                /site_type="other"
                /note="catalytic loop"
                /db_xref="CDD:29154"
     Site       845
                /gene="ERBB2"
                /site_type="active"
                /inference="non-experimental evidence, no additional
                details recorded"
                /note="Proton acceptor (By similarity)."
     Region     848..850
                /gene="ERBB2"
                /region_name="Helical region"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     851..855
                /gene="ERBB2"
                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Region     858..861
                /gene="ERBB2"
                /region_name="Beta-strand region"
                /experiment="experimental evidence, no additional details
                recorded"
     Site       order(863..868,875..879,882..892)
                /gene="ERBB2"
                /site_type="other"
                /note="activation loop"
                /db_xref="CDD:29154"
     Region     886..888
                /gene="ERBB2"
                /region_name="Helical region"
                /experiment="experimental evidence, no additional details
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recorded"
Region 891..896
/gene="ERBB2"
/region_name="Helical region"
/experiment="experimental evidence, no additional details recorded"
Region 901..916
/gene="ERBB2"
/region_name="Helical region"
/experiment="experimental evidence, no additional details recorded"
Region 924..926
/gene="ERBB2"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"
Region 928..930
/gene="ERBB2"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"
Region 931..937
/gene="ERBB2"
/region_name="Helical region"
/experiment="experimental evidence, no additional details recorded"
Region 949..958
/gene="ERBB2"
/region_name="Helical region"
/experiment="experimental evidence, no additional details recorded"
Region 963..965
/gene="ERBB2"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"
Region 969..981
/gene="ERBB2"
/region_name="Helical region"
/experiment="experimental evidence, no additional details recorded"
Region 983..986
/gene="ERBB2"
/region_name="Helical region"
/experiment="experimental evidence, no additional details recorded"
Region 1020..1022
/gene="ERBB2"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"
Site 1139
/gene="ERBB2"
/site_type="modified"
/inference="non-experimental evidence, no additional details recorded"
/note="Phosphotyrosine; by autocatalysis (By similarity)."
Region 1170
/gene="ERBB2"
/region_name="Variant"
/experiment="experimental evidence, no additional details recorded"
/note="P -> A. /FTId=VAR_016318."
Region 1195..1197

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                     /gene="ERBB2"
                     /region_name="Region of interest in the sequence"
                     /inference="non-experimental evidence, no additional
                     details recorded"
                     /note="Interaction with PIK3C2B (Probable)."
     Site            1196
                     /gene="ERBB2"
                     /site_type="modified"
                     /inference="non-experimental evidence, no additional
                     details recorded"
                     /note="Phosphotyrosine (Potential)."
     Site            1248
                     /gene="ERBB2"
                     /site_type="modified"
                     /inference="non-experimental evidence, no additional
                     details recorded"
                     /note="Phosphotyrosine; by autocatalysis (By similarity)."
ORIGIN
        1 melaalcrwg lllallppga astqvctgtd mklrlpaspe thldmlrhly qgcqvvqgnl
       61 eltylptnas lsflqdiqev qgyvliahnq vrqvplqrlr ivrgtqlfed nyalavldng
      121 dplnnttpvt gaspgglrel qlrslteilk ggvliqrnpq lcyqdtilwk difhknnqla
      181 ltlidtnrsr achpcspmck gsrcwgesse dcqsltrtvc aggcarckgp lptdccheqc
      241 aagctgpkhs dclaclhfnh sgicelhcpa lvtyntdtfe smpnpegryt fgascvtacp
      301 ynylstdvgs ctlvcplhnq evtaedgtqr cekcskpcar vcyglgmehl revravtsan
      361 iqefagckki fgslaflpes fdgdpasnta plqpeqlqvf etleeitgyl yisawpdslp
      421 dlsvfqnlqv irgrilhnga ysltlqglgi swlglrslre lgsglalihh nthlcfvhtv
      481 pwdqlfrnph qallhtanrp edecvgegla chqlcarghc wgpgptqcvn csqflrgqec
      541 veecrvlqgl preyvnarhc lpchpecqpq ngsvtcfgpe adqcvacahy kdppfcvarc
      601 psgvkpdlsy mpiwkfpdee gacqpcpinc thscvdlddk gcpaeqrasp ltsiisavvg
      661 illvvvlgvv fgilikrrqq kirkytmrrl lqetelvepl tpsgampnqa qmrilketel
      721 rkvkvlgsga fgtvykgiwi pdgenvkipv aikvlrents pkankeilde ayvmagvgsp
      781 yvsrllgicl tstvqlvtql mpygclldhv renrgrlgsq dllnwcmqia kgmsyledvr
      841 lvhrdlaarn vlvkspnhvk itdfglarll dideteyhad ggkvpikwma lesilrrrft
      901 hqsdvwsygv tvwelmtfga kpydgipare ipdllekger lpqppictid vymimvkcwm
      961 idsecrprfr elvsefsrma rdpqrfvviq nedlgpaspl dstfyrslle dddmgdlvda
     1021 eeylvpqqgf fcpdpapgag gmvhhrhrss strsgggdlt lglepseeea prsplapseg
     1081 agsdvfdgdl gmgaakglqs lpthdpsplq rysedptvpl psetdgyvap ltcspqpeyv
     1141 nqpdvrpqpp spregplpaa rpagatlerp ktlspgkngv vkdvfafgga venpeyltpq
     1201 ggaapqphpp pafspafdnl yywdqdpper gappstfkgt ptaenpeylg ldvpv
//
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